

Amendments to the Claims

Claim 1 (Currently amended): A method of genetically identifying ~~an animal~~ a marker
correlated with favorable muscle growth and/or meat quality comprising:
obtaining a sample of genetic material from said animal;
assaying for the presence of a ~~polymorphism~~ polymorphic allele in a ~~gene selected from the~~
~~group consisting of: CKM, SCN4 α , and LDH α , wherein the presence of said polymorphism is~~
~~associated with favorable muscle growth and/or meat quality gene; and~~
correlating whether a statistically significant association exists between said polymorphic allele
and favorable muscle growth and/or favorable meat quality in an animal of a particular breed,
strain, population, or group whereby said animal can be characterized for said marker.

Claim 2 (Original): The method of claim 1 wherein said animal is a pig.

Claim 3 (Original): The method of claim 1 wherein said assaying is selected from the group
consisting of: restriction fragment length polymorphism (RFLP), heteroduplex analysis, single-
strand conformational polymorphism (SSCP), denaturing gradient gel electrophoresis (DGGE),
single base extension, mass spectrometry, oligo ligation assay (ligase chain reaction), DNA
sequencing and temperature gradient gel electrophoresis (TGGE).

Claim 4 (Original): The method of claim 1 further comprising amplifying an amount of said
gene or a portion thereof which contains said polymorphism.

Claim 5 (Original): The method of claim 4 wherein said amplification includes selecting a
forward a reverse primer capable of amplifying a region of said gene which contains at least one
polymorphic site.

Claim 6 (Original): The method of claim 1 wherein said gene is the CKM gene.

Claim 7 (Original): The method of claim 6 wherein said gene contains a polymorphic MspAII site.

Claim 8 (Original): The method of claim 7 wherein said polymorphic site is amplified by primers selected from and based upon SEQ ID NO: 7 and SEQ ID NO: 8.

Claim 9 (Original): The method of claim 6 wherein said gene contains a polymorphic BamHI site.

Claim 10 (Original): The method of claim 9 wherein said polymorphic site is amplified by primers selected from and based upon SEQ ID NO: 9 and SEQ ID NO: 10.

Claim 11 (Original): The method of claim 6 wherein said gene contains a polymorphism identified by a 9 base pair insertion/deletion.

Claim 12 (Original): The method of claim 11 wherein said polymorphism is amplified by primers selected from and based upon SEQ ID NO: 11 and SEQ ID NO: 12.

Claim 13 (Withdrawn): The method of claim 1 wherein said gene is SCN4 α .

Claim 14 (Withdrawn): The method of claim 13 wherein said gene contains a polymorphic BsrI site.

Claim 15 (Withdrawn): The method of claim 14 wherein said polymorphic site is amplified by primers selected from and based upon SEQ ID NO: 13 and SEQ ID NO: 14.

Claim 16 (Withdrawn): The method of claim 13 wherein said gene contains a polymorphic PstI site.

Claim 17 (Withdrawn): The method of claim 16 wherein said polymorphic site is amplified by primers selected from and based upon SEQ ID NO: 15 and SEQ ID NO: 16.

Claim 18 (Withdrawn): The method of claim 13 wherein said gene contains a polymorphic SalI site.

Claim 19 (Withdrawn): The method of claim 18 wherein said polymorphic site is amplified by primers selected from and based upon SEQ ID NO: 17 and SEQ ID NO: 18.

Claim 20 (Withdrawn): The method of claim 1 wherein said gene is the LDH α gene.

Claim 21 (Withdrawn): The method of claim 20 wherein said gene contains a polymorphic AclI site.

Claim 22 (Withdrawn): The method of claim 21 wherein said polymorphic site is amplified by a forward and a reverse primer selected from and based upon SEQ ID NO: 19 and SEQ ID NO: 20.

Claim 23 (Original): The method of claim 7 wherein said polymorphic site is a C to T single nucleotide substitution in the 5' UTR region of said gene.

Claim 24 (Original): The method of claim 9 wherein said polymorphic site is a G to T single nucleotide substitution in intron 2 of said gene.

Claim 25 (Original): The method of claim 11 wherein said 9 base pair insertion/deletion is characterized by a nucleotide sequence -TGAGCTTCC- present in allele 1 but not present in allele 2.

Claim 26 (Withdrawn): The method of claim 14 wherein said polymorphic site is a C to G single nucleotide substitution in exon 24 of said gene.

Claim 27 (Withdrawn): The method of claim 16 wherein said polymorphic site is a G to A single nucleotide substitution in exon 11 of said gene.

Claim 28 (Withdrawn): The method of claim 18 wherein said polymorphic site is a G to A single nucleotide substitution in exon 2 of said gene.

Claim 29 (Withdrawn): The method of claim 20 wherein said polymorphic site is a polymorphic base, R, wherein said base is a G or an A in exon 5 of said gene.

Claim 30 (Currently Amended): A method of screening an animal to determine said animal's genetic potential for animal breeding comprising:
obtaining a genetic sample from said animal;
identifying said animal's genotype wherein said genotype has at least one polymorphic site in a gene selected from the group consisting of: CKM, SCN4 α , and LDH α ; and
making genetic assessments based upon the presence of a polymorphism in said gene which is correlated with favorable breeding traits.

Claim 31 (Currently Amended): The method of claim 30 wherein identifying at least one polymorphic site comprises:

amplifying said sample which contains a polymorphism;

generating or destroying a restriction site in said sample;

determining whether a site is cleaved by a specific restriction endonuclease; and

determining whether said sample contains an insertion or deletion, wherein cleavage of a restriction endonuclease site or an insertion or deletion indicates the presence of a polymorphism.

Claim 32 (Original): The method of claim 31 further comprising running gel electrophoresis to identify polymorphism.

Claim 33 (Original): The method of claim 30 wherein said genotype is characterized by at least one polymorphism in the CKM gene.

Claim 34 (Original): The method of claim 33 wherein said polymorphism is identified by cleavage of a MspAII restriction endonuclease site in a region amplified by primers SEQ ID NO: 7 and SEQ ID NO: 8.

Claim 35 (Original): The method of claim 33 wherein said polymorphism is identified by cleavage of a BamHI restriction endonuclease site in a region amplified by primers SEQ ID NO: 9 and SEQ ID NO: 10.

Claim 36 (Original): The method of claim 33 wherein said polymorphism is identified by the presence or absence of a 9 base pair insertion/deletion in a region amplified by primers SEQ ID NO: 11 and SEQ ID NO: 12.

Claim 37 (Withdrawn): The method of claim 30 wherein said genotype is characterized by at least one polymorphic site in the SCN4 α gene.

Claim 38 (Withdrawn): The method of claim 37 wherein said polymorphism is identified by cleavage of a BsrI restriction endonuclease site in a region amplified by primers SEQ ID NO: 13 and SEQ ID NO: 14.

Claim 39 (Withdrawn): The method of claim 37 wherein said site is identified by cleavage of a PstI restriction endonuclease site in a region amplified by primers SEQ ID NO: 15 and SEQ ID NO: 16.

Claim 40 (Withdrawn): The method of claim 37 wherein said polymorphism is identified by cleavage of a SalI restriction endonuclease site in a region amplified by primers SEQ ID NO: 17 and SEQ ID NO: 18.

Claim 41 (Withdrawn): The method of claim 30 wherein said genotype is characterized by a polymorphism in the LDH α gene.

Claim 42 (Withdrawn): The method of claim 41 wherein said polymorphism is identified by cleavage of an AciI restriction endonuclease site in a region amplified by primers SEQ ID NO: 19 and SEQ ID NO: 20.

Claim 43 (Original): The method of claim 30 wherein said animal is a pig.

Claim 44 (Original): The method of claim 30 wherein said breeding traits comprises favorable meat quality, heavy muscling, and/or skeletal muscle cramping disease.

Claim 45 (Currently Amended): A method of genotyping an animal ~~to determine whether it possess a favorable combination of traits for muscle growth and/or meat quality comprising:~~
determining the alleles present in an animal said alleles comprising those which include one or more of the following polymorphic sites: a MspA1I, BamHI, or a 9 bp insertion/deletion in a CKM gene; ~~a BsrI, PstI, or a SalI site in a SCN4 α gene; and an AclI site in a LDH α ,~~ wherein the presence of one alternative of said polymorphic site is associated with favorable muscle growth and/or meat quality.

Claim 46 (Original): The method of claim 45 wherein said animal is a pig.

Claim 47 (Currently Amended): A method of genotyping an animal at a polymorphic locus comprising:
obtaining a genetic sample from an animal;
assaying for the presence of a polymorphism, said polymorphism characterized by the following:

- a) a polymorphism in the CKM gene said polymorphism located in the 5' untranslated reation of said gene ~~(SEQ ID NO: 1)~~ as set forth in SEQ ID NO:1;
- b) a polymorphism in the CKM gene said polymorphism located in intron 2 of said gene ~~(SEQ ID NO: 2)~~ as set forth in SEQ ID NO:2; or

- c) a polymorphism in the CKM gene said polymorphism characterized by a 9 bp insertion/deletion in intron 2 of said gene (~~SEQ ID NO: 2~~); as set forth in SEQ ID NO:2.
- d) ~~a polymorphism in the SCN4 α gene said polymorphism located in exon 24 of said gene (SEQ ID NO: 3);~~
- e) ~~a polymorphism in the SCN4 α gene said polymorphism located in exon 11 of said gene (SEQ ID NO: 4);~~
- f) ~~a polymorphism in the SCN4 α gene said polymorphism located in exon 2 of said gene (SEQ ID NO: 5); or~~
- g) ~~a polymorphism in the LDH α gene said polymorphism located in exon 5 of said gene (SEQ ID NO: 6).~~

Claim 48 (Original): The method of claim 47 wherein said animal is a pig.

Claim 49 (Currently Amended): A method of detecting the presence of haplotypes which is predictive for determining the presence of a gene linked with favorable meat quality in an animal, said method comprising:

- a) analyzing a sample of genetic material from said animal for polymorphisms ~~linked with meat quality traits in the gene CKM, wherein the presence of said polymorphisms are associated with favorable meat quality traits and~~ wherein said polymorphisms are selected from the group consisting of MspAII and a 9 bp insertion/deletion; and
- b) correlating the presence of said polymorphism with the presence of said haplotypes such that said haplotypes are detected.

Claim 50 (Original): The method of claim 49 wherein said haplotypes are 1-1, 1-2 and 2-2.

Claim 51 (Original): The method of claim 49 wherein said animal is a pig.